

SEQUENCE LISTING

<110> Guenther, Catherine <120> Transgenic mice containing RORgamma gene disruptions <130> R-409 <140> US 09/895,840 <141> 2001-06-28 <150> US 60/215,466 <151> 2000-06-29 <150> US 60/221,667 <151> 2000-07-27 <160> 4 <170> FastSEQ for Windows Version 4.0 <210> 1 <211> 2066 <212> DNA <213> Mus musculus <220> <221> misc_feature <222> 1527 <223> n = A,T,C or G<400> 1 ggagggcagc aaggacggca ccaagggagc taccccatgg acagggcccc acagagacac 60 caccggacat ctcgggagct gctggctgca aagaagaccc acacctcaca aattgaagtg 120 atcccttgca agatctgtgg ggacaagtca tctgggatcc actacggggt tatcacctgt 180 gaggggtgca agggcttctt ccgccgcagc cagcagtgta atgtggccta ctcctgcacg 240 cgtcagcaga actgccccat tgaccgaacc agccgcaacc gatgccagca ttgccgcctg 300 cagaagtgcc tggctctggg catgtcccga gatgctgtca agtttggccg aatgtccaag 360 aagcagaggg acagtctaca tgcagaagtg cagaaacaac tgcaacagca gcagcaacag 420 gaacaagtgg ccaagactcc tccagctggg agccgcggag cagacacact tacatacact 480 ttagggetet cagatgggea getaceaetg ggegeeteae etgacetaee egaggeetet 540 gcttgtcccc ctggcctcct gagagcctca ggctctggcc caccatattc caataccttg 600 gccaaaacag aggtccaggg ggcctcctgc caccttgagt atagtccaga acgaggcaaa 660 gctgaaggca gagacagcat ctatagcact gacggccaac ttactcttgg aagatgtgga 720 cttcgttttg aggaaaccag gcatcctgaa cttggggaac cagaacaggg tccagacagc 780 cactgcattc ccagtttctg cagtgcccca gaggtaccat atgcctctct gacagacata 840 gagtacctgg tacagaatgt ctgcaagtcc ttccgagaga catgccagct gcgactggag 900 gaccttctac ggcagcgcac caacctcttt tcacgggagg aggtgaccag ctaccagagg 960 aagtcaatgt gggagatgtg ggagcgctgt gcccaccacc tcactgaggc cattcagtat 1020 gtggtggagt ttgccaagcg gctttcaggc ttcatggagc tctgccagaa tgaccagatc 1080 atactactga cagcaggagc aatggaagtc gtcctagtca gaatgtgcag ggcctacaat 1140 _gccaacaacc_acacagtctt_ttttgaaggc_aaatacggtg_gtgtggagct_gtttcgagcc_1200ttgggctgca gcgagctcat cagctccata tttgactttt cccacttcct cagcgccctg 1260 tgtttttctg aggatgagat tgccctctac acggccctgg ttctcatcaa tgccaaccgt 1320 cctgggctcc aagagaagag gagagtggaa catctgcaat acaatttgga actggctttc 1380 catcatcatc tetgeaagae teategacaa ggeeteetag eeaagetgee acceaaagga 1440 aaactccgga gcctgtgcag ccaacatgtg gaaaagctgc agatcttcca gcacctccac 1500 cccatcgtgg tccaagccgc cttcccncca ctctataagg aactcttcag cactgatgtt 1560

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                            40
Glu Gly Cys Lys Gly Phe Phe Arg Arg Ser Gln Gln Cys Asn Val Ala
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Tyr Ser Cys Thr Arg Gln Gln Asn Cys Pro Ile Asp Arg Thr Ser Arg
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                                        75
Asn Arg Cys Gln His Cys Arg Leu Gln Lys Cys Leu Ala Leu Gly Met
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Ser Arg Asp Ala Val Lys Phe Gly Arg Met Ser Lys Lys Gln Arg Asp
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Ser Leu His Ala Glu Val Gln Lys Gln Leu Gln Gln Gln Gln Gln Gln
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Glu Gln Val Ala Lys Thr Pro Pro Ala Gly Ser Arg Gly Ala Asp Thr
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Leu Thr Tyr Thr Leu Gly Leu Ser Asp Gly Gln Leu Pro Leu Gly Ala
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Ser Pro Asp Leu Pro Glu Ala Ser Ala Cys Pro Pro Gly Leu Leu Arg
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Ala Ser Gly Ser Gly Pro Pro Tyr Ser Asn Thr Leu Ala Lys Thr Glu
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Val Gln Gly Ala Ser Cys His Leu Glu Tyr Ser Pro Glu Arg Gly Lys
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Ala Glu Gly Arg Asp Ser Ile Tyr Ser Thr Asp Gly Gln Leu Thr Leu
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Gly Arg Cys Gly Leu Arg Phe Glu Glu Thr Arg His Pro Glu Leu Gly
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Glu Pro Glu Gln Gly Pro Asp Ser His Cys Ile Pro Ser Phe Cys Ser
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Ala Pro Glu Val Pro Tyr Ala Ser Leu Thr Asp Ile Glu Tyr Leu Val
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Gln Asn Val Cys Lys Ser Phe Arg Glu Thr Cys Gln Leu Arg Leu Glu
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Asp Leu Leu Arg Gln Arg Thr Asn Leu Phe Ser Arg Glu Glu Val Thr
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Ser Tyr Gln Arg Lys Ser Met Trp Glu Met Trp Glu Arg Cys Ala His
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His Leu Thr Glu Ala Ile Gln Tyr Val Val Glu Phe Ala Lys Arg Leu
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360

355

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